

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/391,606

DATE: 03/07/2000
TIME: 13:47:56

Input Set: I391606.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Murdin, Andrew D
2   Dunn, Pamela L
3 <120> TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR PROTECTION AGAINST
4   CHLAMYDIAL INFECTION
5 <130> FILE REFERENCE: 1038-971 MIS:jb
6 <140> CURRENT APPLICATION NUMBER: US/09/391,606
7 <141> CURRENT FILING DATE: 1999-09-07
8 <160> NUMBER OF SEQ ID NOS: 20
9 <170> SOFTWARE: PatentIn Ver. 2.1
10 <210> SEQ ID NO 1
11 <211> LENGTH: 2545
12 <212> TYPE: DNA
13 <213> ORGANISM: Chlamydia pneumoniae
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18   aaaaaacatt atgcttggtt tgtagaaggg attctcaatc gtttgccata acagtttttt 240
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23   tggtttattg gaggaacttt agggggactc agaaaagctg gagactggct tgccacagta 540
24   cgttatgagt atgtcgaagc cttgtcagtt ccagaaatag atgtttcagg gattggccgt 600
25   ggtaatttat taaagttttg gttcgcccaa gcaattgctg ctaactatga tcctaaagag 660
26   gctaatagtt ttacaaatta taaaggattt tccgctctat atatgtatgg catcacagat 720
27   tctctatcat tcagagctta tggggcttac tccaaaccag caaacgataa actcggcagt 780
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43   cagatagaga aagatggaaa tgcgattggg gatgcatatt ttgcaggaca gaacgctagt 1740
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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/391,606

DATE: 03/07/2000
TIME: 13:47:56

Input Set: I391606.RAW

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47      cctgcagatg gttctgatgt tccaaatcca ggaactacag ttggaggctc caagcaacaa 1980
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53      gtgagcgagc gagtctctcc gctgcagcaa gttctatgga tccgagctcg gtaccaagct 2340
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60 <212> TYPE: DNA

61 <213> ORGANISM: Chlamydia pneumoniae

62 <400> SEQUENCE: 2

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67      gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaac 300
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70      ggccgtggta atttattaaa gttttggttc gcccagcaa ttgctgctaa ctatgatcct 480
71      aaagaggcta atagttttac aaattataaa ggattttccg ctctatatat gtatggcatc 540
72      acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600
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75 <211> LENGTH: 1470

76 <212> TYPE: DNA

77 <213> ORGANISM: Chlamydia pneumoniae

78 <400> SEQUENCE: 3

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81      gcagggtcgg aagctaagcc taaagaatct aagaccgatt ctgtagagcg atggagcatc 180
82      ttgcgttctg cagtgaatgc tctcatgagt ctggcagata agctgggtat tgcttctagt 240
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84      acgctcctc caccacgctc tgatgattat aagactcaag cgcaaacagc ttacgatact 360
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86      gtcactaata taaaggatac agcggctact gatgaggaaa ccgcaatcgc tgcggagtgg 480
87      gaaactaaga atgccgatgc aattaaagt ggccgcgcaa ttacagaatt agcgaatat 540
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89      cagactgctc ttctccaatc tgtagcaaac aataacaaag cagctgagct tcttaaagag 660
90      atgcaagata acccagtagt cccagggaaa acgcctgcaa ttgctcaatc tttagttgat 720
91      cagacagatg ctacagcgac acagatagag aaagatggaa atgcgattgg ggatgcatat 780
92      tttgcaggac agaacgctag tggagctgta gaaaatgcta aatctaataa cagtataagc 840
93      aacatagatt cagctaaagc agcaatcgct actgctaaga cacaatagc tgaagctcag 900
94      aaaaagttcc ccgactctcc aattcttcaa gaagcggaac aaatggtaat acaggctgag 960

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PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/391,606

DATE: 03/07/2000
TIME: 13:47:56

Input Set: I391606.RAW

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98      atgttcaata cggaaaatcc tgattctcaa gctgccaac aggagctcgc agcacaagct 1200
99      agagcagcga aagccgctgg agatgacagt gctgctgcag cgctggcaga tgctcagaaa 1260
100     gctttagaag cggctctagg taaagctggg caacaacagg gcataactcaa tgctttggga 1320
101     cagatcgctt ctgctgctgt tgtgagcgca ggagtcctcc cgctgcagca agttctatgg 1380
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111     gcagggtcgg aagctaagcc taaagaatct aagaccgatt ctgtagagcg atggagcatc 180
112     ttgcgttctg cagtgaatgc tctcatgagt ctggcagata agctgggtat tgcttctagt 240
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114     acgcctcctc caccacgctc tgatgattat aagactcaag cgcaaacagc ttacgatact 360
115     atctttacct caacatcact agctgacata caggctgctt tggtagacct ccaggatgct 420
116     gtcactaata taaaggatac agcggctact gatgaggaaa ccgcaatcgc tgcggagtgg 480
117     gaaactaaga atgccgatgc aattaaagt ggcgcgcaaa ttacagaatt agcgaaatat 540
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119     cagactgctc ttctccaatc tgtagcaaac aataacaaag cagctgagct tcttaaagag 660
120     atgcaagata acccagtagt cccagggaaa acgcctgcaa ttgctcaatc tttagttgat 720
121     cagacagatg ctacagcgac acagatagag aaagatggaa atgcgattgg ggatgcatat 780
122     tttgcaggac agaacgctag tggagctgta gaaaatgcta aatctaataa cagtataagc 840
123     aacatagatt cagctaaagc agcaatcgct actgctaaga cacaaatagc tgaagctcag 900
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126     gttggaggct ccaagcaaca aggaagtagt attggtagta ttcgtgtttc catgctgtta 1080
127     gatgatgctg aaaatgagac cgcttccatt ttgatgtctg ggtttcgtca gatgattcac 1140
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130     gctttagaag cggctctagg taaagctggg caacaacagg gcataactcaa tgctttggga 1320
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132     atccgagct                                     1389
133     <210> SEQ ID NO 5
134     <211> LENGTH: 63
135     <212> TYPE: DNA
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141     <211> LENGTH: 18
142     <212> TYPE: DNA
143     <213> ORGANISM: Chlamydia pneumoniae
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MAR 20 2000
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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/391,606

DATE: 03/07/2000
TIME: 13:47:56

Input Set: I391606.RAW

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154           20              25              30
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156           35              40              45
157      Met Lys Tyr Lys Tyr Cys Val Trp Gln Trp Leu Val Gly Lys His Ser
158           50              55              60
159      Gln Val Pro Trp Ile Asn Gly Gln Lys Lys Pro Leu Tyr Leu Tyr Gly
160           65              70              75              80
161      Ala Phe Leu Met Asn Pro Leu Ala Lys Ala Thr Lys Thr Thr Leu Asn
162           85              90              95
163      Gly Lys Glu Asn Leu Ala Trp Phe Ile Gly Gly Thr Leu Gly Gly Leu
164           100             105             110
165      Arg Lys Ala Gly Asp Trp Ser Ala Thr Val Arg Tyr Glu Tyr Val Glu
166           115             120             125
167      Ala Leu Ser Val Pro Glu Ile Asp Val Ser Gly Ile Gly Arg Gly Asn
168           130             135             140
169      Leu Leu Lys Phe Trp Phe Ala Gln Ala Ile Ala Ala Asn Tyr Asp Pro
170      145              150              155              160
171      Lys Glu Ala Asn Ser Phe Thr Asn Tyr Lys Gly Phe Ser Ala Leu Tyr
172           165             170             175
173      Met Tyr Gly Ile Thr Asp Ser Leu Ser Phe Arg Ala Tyr Gly Ala Tyr
174           180             185             190
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180 <211> LENGTH: 490
181 <212> TYPE: PRT
182 <213> ORGANISM: Chlamydia pneumoniae
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187           20              25              30
188      Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
189           35              40              45
190      Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
191           50              55              60
192      Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
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194      Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr

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DATE: 03/07/2000
TIME: 13:47:56

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197				100					105					110			
198	Gln	Ala	Gln	Thr	Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	
199			115					120					125				
200	Asp	Ile	Gln	Ala	Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	
201		130					135					140					
202	Lys	Asp	Thr	Ala	Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	
203	145					150					155					160	
204	Glu	Thr	Lys	Asn	Ala	Asp	Ala	Ile	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	
205				165						170					175		
206	Leu	Ala	Lys	Tyr	Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	
207				180				185					190				
208	Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Thr	Ala	Leu	Leu	Gln	Ser	Val	
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213	225					230					235					240	
214	Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	
215				245						250					255		
216	Gly	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	
217				260				265						270			
218	Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	
219			275					280					285				
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221		290					295					300					
222	Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	
223	305					310					315					320	
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225				325						330					335		
226	Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	
227				340				345						350			
228	Ser	Ile	Arg	Val	Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	
229			355					360					365				
230	Ser	Ile	Leu	Met	Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	
231		370					375					380					
232	Glu	Asn	Pro	Asp	Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	
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PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/391,606

DATE: 03/07/2000
TIME: 13:47:56

Input Set: I391606.RAW

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